

Figure 1(a)

HHV8PEP	-----MTPRSR-LATLGTVILLVCFCAG--AAHSRGDTFQ--
RHESRHADPEP	-----MMITNRTRRLRAWVVI IAIGTAVG--ENVTTPKGAT--
MURH68PEP	-----MYPTVKSMRVAHLTNLLTLLCCLLCHTHLYVCQPTTLR--
BOVINEH4PEP	YKTIILFFALIKVCSFNQTTHTSTTSPSISSTTSSTTSTSKPSNTTSTNSSLAASPQ
ATELINEH3PEP	-----MTLNR---CVLLIVLTFSTACS-----Q--
SAIMIRIPEP	-----MVPNK---HLLLIILSFSTACG-----Q--
EQH2PEP	-----MGVGGGPRVVLCLWCVAALLCQGVAEVVAETTPFA--
EQH5PEP	-----MVAWFLGWGFARLMATLALLCGRVALDESSATPSIPP--
ALCELPEP	-----MAHTGSTVCAFLIFAVLKNVFCQTPTSSEVEDVIPEAN--
EBVPEP	-----MTRRRVLSVVVLLAALACRLGA-----Q--TPEQ--
HHV8PEP	--TSSSPTPPGSSSKAPTKPGEEASGPKSVDFYQFRVCSAS-ITGELFRFNLEQTCPDTK
RHESRHADPEP	--TTAKPTP-GPS--TPTPP--ENPPR-AEAFKFRVCSAS-ATGELFRFNLEKTCPGTE
MURH68PEP	--QPSDMTP-AQDAPTETPEPLSTNTNR--GFYFRVCGVA-ATGETFRFDLDKTCPSQ
BOVINEH4PEP	NTSTSKPSTDNQGTSTPTIPTVTDITAS-KNFYKYRVCSSSSSGELFRFDLDQTCPDTK
ATELINEH3PEP	----TTPASDEN--GKTPAIEK--EYF----K-YRVCSAS-TTGELFRFNLDRACPSTE
SAIMIRIPEP	----TPTTAVEK--NKTQAIYQ--EYF----K-YRVCSAS-TTGELFRFDLDRTCPSTE
EQH2PEP	---THRPEVVAEE--NPANP----FLP----F--RVCGASPTGGEIFRFPLEESCNPTE
EQH5PEP	---THKPAVHHED--NTTNP----FLL----F--RVCGASPTG-EIFRFPLEENCNPTE
ALCELPEP	--TVSDNIIRQQR--NNTAKGIHSDPSA---FPFRVCSAS-NIGDIFRQTSHSCPNTK
EBVPEP	---PAPPATTVQP--TATRQ-----QTS----FPFRVCELS-SHGDLEFRSSDIQCPSFG
HHV8PEP	DKY-HQEGILLVYKKNIVPHIFKVRRYRKIATSVTVYRGLTES--AITNKYELPRPVPLY
RHESRHADPEP	DKT-HQEGILMVFKKNIVPHIFKVRRYRKVATSVTVYRGWTET--AVTGKQEVIRPVQY
MURH68PEP	DKK-HVEGILLVYKINIVPYIFKIRRYRKIITQTLTIWRGLTTS--SVTGKFEMATQAHWE
BOVINEH4PEP	DKK-HVEGILLVLKKNIVPYIFKVRKYRKIATSVTVYRGWSQA--AVTNRDDISRAIPYN
ATELINEH3PEP	DKV-HREGILLVYKKNIVPHIFKVRRYKKIATSVRIFNGWSREGVAITNKWELSRAPVKY
SAIMIRIPEP	DKV-HKEGILLVYKKNIVPYIFKVRRYKKITTSVRIFNGWTREGVAITNKWELSRAPVKY
EQH2PEP	DKD-HIEGIALIYKTNIVPYVFNVRKYRKIMTSTTIYKGWSED--AITNQHTRSYAVPLY
EQH5PEP	DKE-HVEGILLIYKTNIVPYIFNVRKYRKLVTSTTIYKGWSQD--AITNQYTSSFAMPLW
ALCELPEP	DKE-HNEGILLIFKENIVPYVFKVRKYRKIVTTSTIYNGIYAD--AVTNQHVFSSKSVPIY
EBVPEP	TRENHTEGLLMVFKDNIIPYSFKVRSYTKIVTNILIYNGWYAD--SVTNRHEEKFSVDSY
HHV8PEP	EISHMDSTYQCFSSMKVNVNGVENTFTDRDDVNTTVFLQPVEGLTDNIQRYFSQPVIYAE
RHESRHADPEP	EINHMDTTYQCFSSMRVNVNGIVNTYTDRTDFTNQTVFLQPVEGLTDNIQRYFSQPVLYTT
MURH68PEP	EVGDFDSIYQCYN SATMVVNVRQVYVDRDGVNKTVNIRPVDGLTGNIQRYFSQPTLYSE
BOVINEH4PEP	EIS MIDRTYHCF SAMATVINGILNTYIDRDS ENKSVPLQP VAGLTENINRYFSQPLIYAE
ATELINEH3PEP	EINLMDKNYQCHNCMQIEVGNLLNSYCDRDGNNKTVDLKPVDGLTGAITRYVSQPKIFAD
SAIMIRIPEP	EIDIMDKTYQCHNCMQIEVGNMLNSYD RDGNNKTVDLKPVDGLTGAITRYISQPKVFAD
EQH2PEP	EVQMDHYYQCFS AVQVNEG GHVNTYD RDGWN ET AFLKPADGLTSSITRYQSQPEVYAT
EQH5PEP	EARLVDYNYECYNGIQVTENGHLTTYVDRDGYNESVRLVPADGLTSSIRRYHSQPELYVT
ALCELPEP	ETRMDTIYQCYN SLDVTVG NLLVYTDNDG SNMTVDLQPV DGLS NSVRRYHSQPEIHAE
EBVPEP	ETDQMDTIYQCYN AVKMTKDGLTRVYVDRDGVNITVNLKPTGGLANGVRRYASQTELYDA
HHV8PEP	PGWFPGIYRV <u>RTTVNCE</u> IVDMIARSAEPYNYFVTS LGDTVEVSPFCYNESSCST-TPSNK
RHESRHADPEP	PGWFPGIYRV <u>RTTVNCE</u> IVDMIARSAEPYSYFVTALGDTVEVSPFCHNDSTCSV-AEKTE
MURH68PEP	PGWMPGFYRV <u>RTTVNCE</u> IVDMVARSM DPYNYIATALGDSLELSPFQTFDNTS QS-TAPKR
BOVINEH4PEP	PGWFPGIYRV <u>RTTVNCE</u> IVDMYARSVEPYTHFITALGDTIEISPFCHNNSQCTGNSTSR
ATELINEH3PEP	AGWLWGTYKTR <u>RTTVNCE</u> IVEMFARSADPYTYFVTALGDTVEVSPFCDAENSCPN----AS
SAIMIRIPEP	PGWLWGTYR <u>RTTVNCE</u> IVDMFARSADPYTYFVTALGDTVEVSPFCVDVNSCPN----AT
EQH2PEP	PRNLLWSYT <u>RTTVNCE</u> VTEMSARSMKPF EFFVTSVGD TIEMS PFLKENGTEPE--KILK
EQH5PEP	PRNLLWSYT <u>RTTVNCE</u> VIDMTARSHKPF EYFVTASGDSIETSPFFYT-NASR-----R
ALCELPEP	PGWLLGGYRR <u>RTTVNCE</u> VTETDARAVPPFRYFITNIGDTIEMSPFWSKAWNETEFS--GE
EBVPEP	PGWLIWYTR <u>RTTVNCL</u> ITDMMAKSNSPFDFFVTTTGQTVEMSPFYDGKNKETF----HE

Figure 1(b)

HHV8PEP	NGLSVQVVLNHTVVTYSDRGTSPTQNRIFVETGAYTLWSASESKTTAVCPALWKTFFPR
RHESRHADPEP	NGLGARVLNTYTMVDFATR--APTETRVFADSGEYTVSWKAEDPKSAVCALTWKTFFPR
MURH68PEP	ADMVRREVKNYKFVDYNNRGTAAPAGQSRTFLETSPATYSWKTATROTATCDLVHWKTFFPR
BOVINEH4PEP	DATKVWIEENHQTVDYERRG-HPTKDKRIFLKDEEYTLISWKAEDRERAICDFVIWKTFFPR
ATELINEH3PEP	DVLSSQVDFNHTVVDYGNRATSQQHGKRIFAHTLDYSVSWEAINKTTSVCSMVFWKGFQR
SAIMIRIPEP	DVLSVQIDLNHTVVDYGNRATSQQHKKRIFAHTLDYSVSWEAVNKSASVCSMVFWKSFQR
EQH2PEP	RPHSIQLLKNYAVTKYGVGLGQADNATRFFAIFGDYSLSWKATTENSSYCDLILWKGFNS
EQH5PEP	VP--VQVLYNYSVTDYGVGLSGGENVTRFFATLNDFSISWKAATENSSYCPLVLWKGFPS
ALCELPEP	PDRTLTVAKDYRVVDYKFRGTQPGHTRIFVDKEEYTLSWAQQFRNISYCRWAHWKSFND
EBVPEP	RADSFHVRTNYKIVDYDNRGTNPQGERRAFLDKGTYTTLWKLENR-TAYCPLQHWQTFDS
HHV8PEP	SIQTTTHEDSFHFVANEITATFTAP--LTPVANFTDTYSCLTSDINTTLNASKAKLSTH
RHESRHADPEP	AIQTTHEASYHFVANDVTATFTSP--LSEVANFTGTYSCLDEVIQKTLNDTIKKLSDTH
MURH68PEP	AIQTAHEHSYHFVANEVTATFTNP--LTEVENFTSTYSQVSDQINKTISEYIQKLNSY
BOVINEH4PEP	AIQTIHNESFHFVANEVTASFLTSNQEETELRGNTIELNCMNSTINETLEETVKKFNKSH
ATELINEH3PEP	AIQTEHDSTYHFIANEITAGFSTS--KETLASFSSEYSCLMSDINSTLTDKIGRVNNTH
SAIMIRIPEP	AIQTEHDLTYHFIANEITAGFSTV--KEPLANFTSDYNCLMTHINTTLEDKIARVNNTH
EQH2PEP	AIQTQHNSSLHFIANDITASFSTP--LEEEAN-FNETFKCIWNNTQEEIQKKLKEVEKTH
EQH5PEP	AIQTKHEKSYHFIADAVTASFTTP--LTDETSYFNNTTYQCAWQDIEGETIQRFPVSKTH
ALCELPEP	AIKTEHGKSLHFVANDITASFYTP--NTQTREVLGKHVCLNNTIESELKSRLAKVNDTH
EBVPEP	TIATETGKSIHFVTDEGTSSFVTN--TTVGIELPDAFKCIEEQVNKTMEKYEAVQDRY
HHV8PEP	VP-NGTVQYFHTTGGLYLVWQPMASAINLTHAQ-GDSGNPTSSPPPSASP-----M
RHESRHADPEP	VT-NGSAQYYKTEGGLFLLWQPLTPLSLVDEMRLNG---TTPAP---P-----A
MURH68PEP	VA-SGKTQYFKTDGNLYLIWQPLEHPEIEDID--EDSDPEPTPAP---P-----K
BOVINEH4PEP	IR-DGEVKKYKTNGGLFLIWQAMKPLNLSEHT-----N-YTIER---N-----N
ATELINEH3PEP	VP-NGTAQYFKTEGGMILVWQPLTAIELEEAIEEAMIEATTVSPTPLS-----T
SAIMIRIPEP	TP-NGTAIEYYQTEGGMILVWQPLIAIELEEAIEEAMLEATTSPVTPSAP-----T
EQH2PEP	RP-NGTAKVYKTTGNLYIVWQPLIQIDLLDTHAKLYNLTNATASPTSTP-----
EQH5PEP	AR-NGSVQIYKTSGNLYVWQPLVQLDLLAAHAKTINSTDNSTSPPTAPN-----TT
ALCELPEP	SP-NGTAQYYLTNGGLLLVWQPLVQKLLDAKGLLDVAVKKQONTT---T-----T
EBVPEP	TKGQEAITYFITSGGLLLAWLPLTPRSLATVKNLTELTTPTSSPPSSPSPAPSAAARGST
HHV8PEP	TTSASRRKRRSASTAAAGG---GGSTDN-----LSYTQLQFAYDKLRDGINQVLEELSRA
RHESRHADPEP	TTSTVSRVRRSVNTNEQ-----ATDN-----LAAPQLQFAYDKLRASINKVLEELSRA
MURH68PEP	STRRKREAADNGNSTSEVS---KGSENP-----LITAQIQFAYDKLTTSVNNVLEELSRA
BOVINEH4PEP	KTGNKSRQKRSVDTKTFQG-----AKG-----LSTAQVQYAYDHLRTSMNHILEELTKT
ATELINEH3PEP	AHLTSRRTGRRKRDVSAG-----SENS-----VLLAQIQAYDKLRQSINNVLEELAIT
SAIMIRIPEP	SSSRSKRAIRSIRDVSAG-----SENN-----VFLSQIQAYAYDKLRQSINNVLEELAIT
EQH2PEP	-TTSPPRRRRDTSVSSGGG---NNGDNSTKEESVAASQVQFAYDNLRSINRVLGELSRA
EQH5PEP	TSTSSRRKRRTGTGNATNN---SSSNSSMEENLATSQVQFAYDQLRSINRVLEQLSRV
ALCELPEP	TTTSRRRQRRSVSSGIDDV---YTAEST-----ILLTQIQFAYDTLRAQINNVLLEELSRA
EBVPEP	PAAVLRRRRRDAGNATTPVPPTAPGKSLGTLNPNPATVQIQFAYDSLRRQINRMLGLLARA
HHV8PEP	WCREQVRDNLMWYELSKINPTSVMTAIYGRPVSAKFVGDAISVTECINVDQSSVNIHKSL
RHESRHADPEP	WCREQVRDNTYMWYELSKINPTSVMTAIYGRPVSAKFVGDAISVTDCAVDQASVSIHKSL
MURH68PEP	WCREQVRDNTLMWYELSKVNPTSVMSAIYGRPVAARYVGDAISVTDICIYVDQSSVNIHQSL
BOVINEH4PEP	WCREQQKDNLMWYELSKINPTSVMAAIYGRPVAVKAMGDAFMVSECINVDQASVNIHKSM
ATELINEH3PEP	WCREQVRQTMWYELIAKINPTSVMTAIYGRPVSALALGDVISVTECINVDQTSVSIHKSL
SAIMIRIPEP	WCREQVRQTMWYELIAKINPTSVMTAIYGRPVSRAKALGDVISVTECINVDQSSVSIHKSL
EQH2PEP	WCREQYRASLMWYELSKINPTSVMSAIYGRPVSALIGDVVSVDICISVDQKSVFVHKNM
EQH5PEP	WCQNQYRASLMWYELSKINPTSVMSAIYGRPVSALVGDVVQISDCITVDQESVFVHRNL
ALCELPEP	WCREQHRASLMWYELSKINPTSVMSAIYGRPVSALRIGDVISVSHCVVDQDSVSLHRSM
EBVPEP	WCLEBQRQNMVLRRLTKINPTTVMSAIYGRKAAKRLGDVISVSCVPVQATVTLLRKS

Figure 1(c)

HHV8PEP	RTN---SKDVCYARPLVTFKFLNSSNLTGQLGARNEIILTNNQVETCKDTCEHYFITRN
RHESRHADPEP	RTS---TPGMCYSRPPVTFRFLNSTTLFKGQLGPRNEIILTDNQVEACKETCEHYFIASN
MURH68PEP	RLQH--DKTTCYSRPRVTFKFINSTDPLTGQLGPRKEIILSNTNIETCKDESEHYFIVGE
BOVINEH4PEP	RTD---DPKVCYSRPLVTFKFVNSTATFRGQLGTRNEILLTNTHVETCRPTADHYFFVKN
ATELINEH3PEP	KTT---NNDVCYSRPPVTFKFVNSSQLFKGQLGARNEILLSESLVENCHQNAEHFFTAKN
SAIMIRIPEP	KTE---NNDICYSRPPVTFKFVNSSQLFKGQLGARNEILLSESLVENCHQNAETFFTAKN
EQH2PEP	KVPG--KEDLCYTRPVVGFKFINGSSELFAGQLGPRNEIVLSTSQVEVCQHSCEHYFQAGN
EQH5PEP	RVPG--SKDLCYTRPVVGFKFINGSSELFVQQLGARNEILLSTNLVEVCQHSCEHYFQGGN
ALCELPEP	RVPGDKTHECYSRPPVTFKFINDSHLYKGQLGVNNEILLTTTAVEICHENTEHYFQGGN
EBVPEP	RVPG--SETMCYSRPLVSFSFINDTKTYEGQLGTDNEIFLTKKMTEVCQATSQYYFQSGN
HHV8PEP	ETLVYKDYAYLRTINTTTDISTLNTFIALNLSFIQNIIDFKAIELYSSAEKRLASSVFDLET
RHESRHADPEP	VTYYYKDYVFKKINTSEISTLGTFIALNLSFIENIDFRVIELYSRAEKKLSGVSVDIET
MURH68PEP	YIYYKKNYIFEEKLNLSIATLDTFIALNISFIENIDFKTVELYSSTERKLASSVFDIES
BOVINEH4PEP	MTHYFKDYKFKVKTMDTNNISTLDTFLTLNLTFIENIDFKTVELYSETERKMAS-ALDLET
ATELINEH3PEP	ETYHFKNYLHVETLPLTNISTLDTFLALNLTFIENIDFKAVELYSSGERKLAN-VFDLET
SAIMIRIPEP	ETYHFKNYVHVETLPLVNISTLDTFLALNLTFIENIDFKAVELYSSGERKLAN-VFDLET
EQH2PEP	QMYKYKDYVYSTLNLTDPTLHTMITLNLSLVENIDFKVIELYSKTEKRLSN-VFDIET
EQH5PEP	HIYKYKNYEVYSTMNLTDPVTLHTMITLNLSLVENIDFQVIQLYSQKEKKLSN-VFDIET
ALCELPEP	NMYFYKNYRHVKTMVGDVATLDTFMVLNLTLENIDFQVIELYSREEKRMST-AFDIET
EBVPEP	EIHVYNDYHHFKTIELDGIATLQTFISLNTSLIENIDFASLELYSRDEQRASN-VFDLEG
HHV8PEP	MPREYNYYTHRLAGLREDLNTIDMNERFVRDLSEIVADLGGIGKTVVNVASSVVTLCG
RHESRHADPEP	MPREYNYYTQRLAGLREDLNTIDLNRDLRLARDLSEIVADLGDVGRVTVVNVASSVITLFG
MURH68PEP	MPREYNYYTSLAGIKKDELNTIDYNRDLVQDLSDMMADLGDIGRSVVNVSSVVTFFS
BOVINEH4PEP	MPREYNYYTQKLASLREDLNTIDLNRDLVQDLSEMADLGDIGKVVVNTFSGIVTVFG
ATELINEH3PEP	MPREYNYYAQSIISGLRKDFDNSQRNDRDRIIQDFSEILADLGSIGKVIVNIASSAFSLFG
SAIMIRIPEP	MPREYNYYAQSIISGLRKDFDNSQRNDRDRIIQDFSEILADLGSIGKVIVNVASGAFSLFG
EQH2PEP	MPREYNYYTQNLNGLRKDLDDSIDHGRDSFIQTLGDIQDLGTIGKVVVNVASGVFSLFG
EQH5PEP	MPREYNYYTQNLKGLRKDLDDSIDHGRDSFIQFLGDLVQDLVPGDVIVNVASGVFSLFG
ALCELPEP	MPREYNYYTQRTVGLRDLTD-LATNRNQFVDAFGSLMDDLGVVGKTVLNAVSSVATLFS
EBVPEP	IFREYNFQAQNIAGLRKDLDNAVSNGRNQFVDGLGELMDSLGSVGQSITNLVSTVGGFLS
HHV8PEP	SLVTGFINFIKHPLGGMMLMIIIVIAIILIIIFMLSRRTNTIAQAPVKMIYP---DVDRAA
RHESRHADPEP	SIVSGFINFIKSPFGGMLMILVIVAVVLIVFALNRRTNAIAQAPIRMIYP---DIDKMQ
MURH68PEP	SIVTGFIFFTNPLGGIFILLIIGGIIIFLVVVLNRRNSQFHDAPIKMLYPSVENYAARQA
BOVINEH4PEP	SIVGGFVSFFTNPIGGVTIILLIVVVFVVFIVSRRTNNMNEAPIKMIYP---NIDKAS
ATELINEH3PEP	GIVTGILNFIKNPLGGMFTFLLVGAIILVILLVRRTNMNSQAPIRMIYP---DIEKSR
SAIMIRIPEP	GIVTGILNFIKNPLGGMFTFLLVGAIILVILLVRRTNMNSQAPIRMIYP---DVEKSK
EQH2PEP	SIVSGVISFFKNPFGGMLLIVLIIAGVVVYLFMTSRRSIYSAPIRMLYP---GVERAA
EQH5PEP	SIVSGVISFLKNPLGAILTIALIVGGIIVLYLFIITRSRTVYQAPIRMLYP---EVDRAV
ALCELPEP	SIVSGIINFIKNPFPGGMLLFLGLIAAVVITVILLNRKAKRFAQNPVQMIYP---DIKTIT
EBVPEP	SLVSGFISFFKNPFGGMLLIVLVAGVVILVISLTRTRTQMSQQPVQMLYP---GIDELA
HHV8PEP	PP-----SGGAPTREEIKNILLGMHQLQ---ERQKADDLKKSTPSVFQRTANGLR
RHESRHADPEP	P-----SGGKVDQEQIKNLAGMHQLQ---EERRRLDEQQRSAFSLFRASDGLK
MURH68PEP	PPPYSA---SPPAIDKEIKRILLGMHQLVHQ---EKEAQKQLTNSGPTLWQKATGFLR
BOVINEH4PEP	EQE-----NIQPLPGEEIKRILLGMHQLQ---SEHGKSEEEASHKPGFLQLLGDGLQ
ATELINEH3PEP	S-----SVTPTEPEVIKQILLGMHNMQQ---EYKKREEHKASQPSFLKRATDAFL
SAIMIRIPEP	S-----TVTPMEPETIKQILLGMHNMQQ---EAYKKKEEQRAARPSIFRQAAETFL
EQH2PEP	QEP-----GAHPVSEDQIRNLMGMHQQFQQRQRAEEEARREEEVKGKRTLFEVIRDSAT
EQH5PEP	QQ-----NVQPIPEDQVRSILLAMHQQFQQQQQQQQQQQEEHTQ--RRSIFDTIRESTS
ALCELPEP	SQREEL---QVDPISKHELDRIMLAMHDYHASK--QPESKQDEEQGSTTSGPADWLNKAK
EBVPEP	QQHASGEGPGINPISKTELQAIMLALHEQNQ-----EQKRAAQRAAGPSVASRALQAAR

Figure 2

336270 "445500"

ATGGCAGGTA	GCTTAAAACT	TAGGGGATCT	GTTCTAGCAC	TGTGGTACCT	GTATCAGGTG	60
GCTCTTTATT	CACCTAGTAT	AGCAGAGACC	GGTGTAACCT	CACCTCCAAA	TACAGCGACC	120
TGGTCTACTG	AATCGCCGCT	AACAGGTCAC	TATGGAACAC	ACGATTCAAG	CCATGGTGAA	180
AGAGGAAACA	ACGAAAACAG	AGATTTCAGAA	GAGCAAAATA	AAAACATTTA	TGGATCGCCT	240
TCTACGTTTC	CTTACAGAGT	ATGCAGTGCC	TCCGGAGTTG	GAGATGTCTT	TAGATTTCAG	300
ACCGACCATG	TGTGTCCCGA	TGCCAGTGAT	ATGGTACACA	GTGAGGGGAT	TCTACTAATT	360
TACAAACAGA	ACATTATTCC	ATTTATGTTT	AGAGTTAGGA	AATATAGAAA	AGTTGTTACA	420
ACAAGTACTG	TCTACAATGG	TATTTATTCT	GACTCTATTA	CCAACCAACA	TACTTTCTAT	480
AAATCAATCG	AACCTTGGGA	GACAGAAAAG	ATGGACACAA	TATATCAGTG	TTTTAATTCT	540
TTAAGACTAA	ACACAGGTGG	AAATCTGCTT	ACTTATGTAG	ATAGAGATGA	TATAAATATG	600
ACAGTGTTTC	TGCAACCTGT	TGACGGTGTG	ACGCCCGATG	TGAAGAGGTA	TGGCAGTCAA	660
CCAGAGCTGT	ACCTTGAACC	TGGCTGGTTT	TGGGGTAGTT	ATAGAAGACG	AAC TACAGTG	720
AACTGTGAAC	TAATGGACAT	GTTTGCAAGA	TCAAATCCTC	CATTTGATTT	CTTTGTTACA	780
GCTACAGGTG	ATACGGTGGA	AATGTCTCCA	TTTTGGAGTG	GTGAAGATGA	TCATGAAAAT	840
AAGATGCACG	AGAAGCCATG	GTTTGTTAGT	GTGATAAATA	ACTACAAGGT	GGTGGACTAT	900
CAAAACAGAG	GGACTGTACC	CCTTGGAATA	ACAAGGATAT	TTCTAGATAG	GGAAGAGTAT	960
ACATTATCTT	GGGAAAAGCA	TCTAAAAAAT	ATGTCATATT	GTCCACTAAC	ATTATGGAAA	1020
GCATTTTACA	ATGGAATCCA	GACGGAGCAT	TCAGGCTCAT	ATCATTTTGT	AGCCAATGAC	1080
ATCAGACGCT	CATTACAAC	TAGTAAAGAA	GACATGAAAG	AGTTCAATAC	GACATATCAT	1140
TGTCTCAACG	AGGAAATAAA	GGCAGAAATA	GAGAAGAAAT	ATGCAAAAGT	AAACTCAACT	1200
CACTCTAAAT	ATGGAGATCT	GAAATACTTT	AAAACAGATG	GGGGTCTCTA	TTTAGTCTGG	1260
CAACCTCTTA	TTCAAAACAG	GCTTCTTGAT	GCTAAGAACA	AACTGAACAA	TGAGACTTAT	1320
TCCAGGAGAT	CACGACGTCA	GGCAGAATCT	ACTACTGACC	CAATGATGGA	GATGACTGGA	1380
AATGGAGCAG	GTGGAGAATA	TAGCAGTGAA	AATTCATCA	CGGTGGCGCA	GGTGCAGTAT	1440
GCCTATGACA	ATCTTCGTAT	CAGAATAAAT	AACATTTTGG	AAGATTTGTC	AAAGGCATGG	1500
TGTCGTGAGC	AGCATAGAGC	TGCTCTGGTG	TGGAATGAGC	TCAGCAAGAT	TAATCCCACA	1560
AGCGTCATGA	ACTGATTTA	CAATAGACCC	GTATCAGCCA	AAAGAATAGG	AGATGTCATT	1620
TCAGTCTCTA	ACTGTATTGT	GGTAGACCAA	ACCAGTGTCT	CATTACATAA	AAGTCTCAGG	1680
CTTCTCAGTG	CATCGGATGA	AAAGTGCTTC	TCTAGACCTC	CAGTGACATT	TAAGTTTATG	1740
AATGACAGTA	CTATTTACAA	AGGGCAACTA	GGAGTCAATA	ATGAGATTCT	CTTAACCACA	1800
ACATACCTTG	AAACATGTCA	GGAAAACACT	GAGTATTACT	TTCAGGCAAA	GACAGACATG	1860
TACATTTACA	AAAACATATGA	GCATTTGAAG	ACTGTGCCTT	TATCTTCGAT	CACCACACTA	1920
GATACATTTA	TAGCCCTTAA	TTTTACACTA	TTGGAGAATG	TTGACTTTAA	AGTCATTGAA	1980
CTTTATACCA	GGGACGAGAA	GAGGCTTAGT	AATGTCTTTG	ACATTGAAAC	AATGTTTAGG	2040
GAATATAACT	ACTATGCTCA	GAGGGTCAGT	GGCCTCAGAA	AGGATTTGCT	GGATCTAAGC	2100
ACCAATAGAA	ATCAATTTGT	GGATGCATTT	GGTAGTCTTA	TGGATGATTT	GGGTGCTGTT	2160
GGGCAGACAG	TTGTAAATGC	TGTAAGTGGT	GTGGCTACGC	TGTTTAGCTC	AATTGTAACA	2220
GGATTTATTA	ATTTCATTA	AAACCCATTT	GGTGGAAATG	TAATGATTAT	TGTTGTTATT	2280
GGTGTGCTAT	TTGCCATCTA	CTTTCTGACC	AAAAAGACGA	AGATATATGA	GACGGCACCG	2340
ATTAAGATGA	TTTATCCTGA	AATTGACAAG	CTGAAAGAAC	GTGAGGGAAA	ATCAGAAATA	2400
GCACCAATCA	GTGAAGAAGA	GCTGGAGAGA	ATTGTACTTG	CTATGCACAT	CCATCAACAA	2460
AATTCACATA	TGGAAACAAA	AACAAGGAAG	GATCCCAAAG	ACAGCATATT	AACAAGGGCA	2520
CAAAATATGC	TACGCAAAAG	ATCAGGATAT	TCTAATTTAA	AAAATGCTGA	ATCTGTGGAG	2580
ATGTTAAACA	CTTTATAA					2598

Figure 3

MAGSLKLRGS	VLALWYLYQV	ALYSLSIAET	GVTSPPTAT	WSTESPLTGH	50
YGTHDSSHGE	RGNNENRDSE	EQNKNIYGSP	STFPYRVCSA	SGVGDVFRFQ	100
TDHVCPDASD	MVHSEGILLI	YKQNIIPFMF	RVRKYRKVVT	TSTVYNGIYS	150
DSITNQHTFY	KSIEPWETEK	MDTIYQCFNS	LRLNTGGNLL	TYVDRDDINM	200
TVFLQPVDGV	TPDVKRYGSQ	PELYLEPGWF	WGSYRRRTTV	NCELMDMFAR	250
SNPPFDFFVT	ATGDTVEMSP	FWSGEDDHEN	KMHEKPWFVS	VINNYKVVDY	300
QNRGTVPLGK	TRIFLDREEY	TLSWEKHLKN	MSYCPLTLWK	AFYNGIQTEH	350
SGSYHFVAND	ITASFTTSKE	DMKEFNNTYH	CLNEEIKAEI	EKKYAKVNST	400
HSKYGDLKYF	KTDGGLYLVW	QPLIQNRLLD	AKNKLNNETY	SRRSRRQAES	450
TTDPMMEMTG	NGAGGEYSSE	NSITVAQVQY	AYDNLIRIRIN	NILEDLSKAW	500
CREQHRAALV	WNELSKINPT	SVMSMIYNRP	VSAKRIGDVI	SVSNICIVVDQ	550
TSVSLHKSLR	LLSASDEKCF	SRPPVTFKFM	NDSTIYKGQL	GVNNEILLTT	600
TYLETCQENT	EYYFQAKTDM	YIYKNYEHLK	TVPLSSITTL	DTFIALNFTL	650
LENVDFKVIE	LYTRDEKRLS	NVFDIETMFR	EYNYAQRVS	GLRKDLLDLS	700
TNRNQFVDAF	GSLMDDLGA	GQTVVNAVSG	VATLFSSIVT	GFINFIKNPF	750
GGMLMIIVVI	GVLFAIYFLT	KKTKIYETAP	IKMIYPEIDK	LKEREKGKSEI	800
APISEEEELER	IVLAMHIHQ	NSHMETKTRK	DPKDSILTRA	QNMLRKRSYG	850
SNLKNAESVE	MLNTL				865

# Figure 4

pGHV-gpB DNA.txt	-----AATCT	TCGTATCAGA	ATAAATAACA	25
pGHV1 DNA. (641-1300)	CGCCGCCGTC	CGGCTCCACG	GTGGTGCGGC	688
		T G C GA A C		
pGHV-gpB DNA.txt	TTTTGGAAGA	TTTGTCAAAG	GCATGGTGTC	75
pGHV1 DNA. (641-1300)	GCCCCGAGTA	CTCG-CAGGG	GCGCAACTTC	737
	GA A T G CA G C	TC	G G A T G TGCT	
pGHV-gpB DNA.txt	CTGGTGTGGA	ATGAGCTCAG	CAAGATTAAT	125
pGHV1 DNA. (641-1300)	CT---T-CA	AGGAGAACAT	C--G-CC--C	776
	CT T A A GAG CA C G	C CACAAG	TCA G C	
pGHV-gpB DNA.txt	GATTTACAAT	-AGACCCGTA	TCAGC-CAAA	172
pGHV1 DNA. (641-1300)	CATCTACTAC	AAGAACGTCA	TCGTACAGAC	826
	AT TAC A AGA C A TC C C A G T G G CA T			
pGHV-gpB DNA.txt	CAGTCTCTAA	C-TGTATTG-	-TGGTAGACC	219
pGHV1 DNA. (641-1300)	ACGCGGCCAT	CACGAACCGC	TTCACAGACC	876
	G C A C G A G T AGACC		GT C C T CA	
pGHV-gpB DNA.txt	AAAAGTCTCA	GGCTTCTCAG	TGCATCGGAT	269
pGHV1 DNA. (641-1300)	GAGA-TCACG	GACGTGATCG	ACCGCCG--C	922
	A A TC C C T G C CG G AAGTGC	TCTC A A		
pGHV-gpB DNA.txt	TCCAGTGACA	T--TTAA-GT	TTATGA-ATG	314
pGHV1 DNA. (641-1300)	CCGAGT-ACG	TGCGCAACAA	CCACAAGGTG	971
	C AGT AC T AA A A TG AC G T C AG			
pGHV-gpB DNA.txt	GCAACTAG--	GAGTCAATAA	TGAGATTCT-	354
pGHV1 DNA. (641-1300)	GAACCCCGTC	GAGGTGGACC	TGCGCCCTC	1021
	G A C GAG TG G CT CT AAC C C			
pGHV-gpB DNA.txt	TAC-C--TTG	AAACA-TGTC	-AGGAAA---	395
pGHV1 DNA. (641-1300)	CCCGCGGCTG	GCACACCACC	AACGACACCT	1071
	C C TG ACA C A GA A ACAC AG C C			
pGHV-gpB DNA.txt	GGCAAAGACA	GACATGTACA	TTTACAAAAA	439
pGHV1 DNA. (641-1300)	GGCTTCTAC-	CACACGGGCA	CCTCCGTCAA	1120
	GGC AC ACA G CA T C AA CT AT GAG A TG			
pGHV-gpB DNA.txt	AGAC-----	--TGTGCCTT	TA-----TCT	476
pGHV1 DNA. (641-1300)	AGGCGCGCTC	CGTGTACCCC	TACGACTCCT	1170
	AG C TGT CC TA CT TCG C CAC G AC			
pGHV-gpB DNA.txt	ATT---TATA	GCCCTTAATT	TTAC--ACTA	521
pGHV1 DNA. (641-1300)	ATTGTGTACA	TGTCCTCCCTT	CTACGGCCTG	1220
	ATT TA A C TT TAC T GAG G AC A			
pGHV-gpB DNA.txt	AGTCATGAA	CTTTATACCA	GGG----ACG	564
pGHV1 DNA. (641-1300)	GCACATCG-G	CTACGCGCCC	GGGCGCTTCC	1269
	CAT G CT CC GGG C AG G GG A TA A			
pGHV-gpB DNA.txt	GTCTTTGACA	TTGAAACAAT	G-----	585
pGHV1 DNA. (641-1300)	CCCATCGAC-	CTGGACTCGC	GCCTCCGCGC	1300
	C T GAC TG A G			

# Figure 5

pGHV-gpB prot	-----N LRI-----	4
PGHV1Prot. (491-850)	PAAPAAARRA RRSPPAGTP EPPAVNGTGH LRITTSAEF ARLQFTYDHI LRI	540
pGHV-gpB prot	--RINNILED LSKAWCREQH RAALVWNELS KINPTSVMSM IYNRPVSAKR	52
PGHV1Prot. (491-850)	QAHVNDMLGR IAAAWCELQN KDRTLWSEMS RLNPSAVATA ALGQRVSAARM N L AWC Q W E S NP V VSA	590
pGHV-gpB prot	IGDVISVSNC IVVDQTSVSL HKSLRLLSAS DEKCFSRPPV TFKFMNDSTI	102
PGHV1Prot. (491-850)	LGDVMAISRC VEV-RGGVYV QNSMR-VPGE RGTCTSRPLV TFE-HNGTGV GDV S C V V S R C SRP V TF N	637
pGHV-gpB prot	YKQQLGVNNE ILLTTTYLET CQENTYYFQ AKTDMYIYKN YEHLKTVPLS	152
PGHV1Prot. (491-850)	IEGQLGDDNE LLISRDLEP CTGNHRRYFK LGSGVYYED YNYVRMVEVP GQLG NE L E C N YF Y Y V	687
pGHV-gpB prot	SITTLDTFIA LNFTLLENVD FKVIELYTRD E----- --KR----	185
PGHV1Prot. (491-850)	--ETISTRVT LNLTLLEDRE FLPLEVYTRE ELADTGLLDY SEIQRRNQLH T LN TLE F E YTR E R	735
pGHV-gpB prot	-----	185
PGHV1Prot. (491-850)	ALKFYDIDRV VKVDHNVVLL RGIANFFQGL GDVGAAVGKV VLGATGAVIS	785
pGHV-gpB prot	-----LS NVF-----	190
PGHV1Prot. (491-850)	AVGGMVSFLS NPPGALAIGL LVLAGLVAAF LAYRHISRLR RNP MKALYPV LS N F	835
pGHV-gpB prot	-----DI E--TM	195
PGHV1Prot. (491-850)	TTKTLKEDGV DEGDV	850

## Figure 6

pGHV-gpB DNA.txt	-----	-----	-----	-----	-----	
pGHV2 DNA.txt	CCAGCATAAT	GATAGCCAAT	AATCTGTGTT	ACTCTACCCT	GATCTTAAAT	50
pGHV-gpB DNA.txt	-----	-----	-----	-----	-----AATCT	5
pGHV2 DNA.txt	GACGAGGACG	TGACGGGGAT	CGACGAGAAA	GATATTCTGA	CGGTGCATGT	100
					AT T	
pGHV-gpB DNA.txt	TCGTATCAGA	ATA-AAT-AA	CATTTTGGAA	GATTGTGCAA	AGGCATGGTG	53
pGHV2 DNA.txt	--AAACAAGA	ATACCGTGTA	CAGGTTTCG-T	TAGGAG-CAG	CGTCAGGGAG	146
	A AGA ATA	T A CA	TT G	A G CA	G CA GG G	
pGHV-gpB DNA.txt	TC-GTGAGCA	GCATAGAGCT	GCTCTGGTGT	GGAATGAGCT	CAGCAAGATT	102
pGHV2 DNA.txt	TCTATACTCG	GCAC---GCT	GCT---GTCT	AG-ATG-GCT	CAGGAAGAGA	188
	TC T C GCA	GCT	GCT	GT T G	ATG GCT	CAG AAGA
pGHV-gpB DNA.txt	AATCCACAA	GCG-TCATGA	GCATGATTTA	CAAT-AGACC	CGTAT-CAGC	149
pGHV2 DNA.txt	AA---GGAA	GTGAAGGCGC	GCATGAAACG	CTGTGAGGAC	CCTATGTGG	234
	AA AA G G	G	GCATGA	C T AG	C C TAT T	
pGHV-gpB DNA.txt	CAAAAGAATA	GGAGATGTCA	TTTCAGTCTC	TAACGTGATT	GTGGTAGACC	199
pGHV2 DNA.txt	C-ACTG-AT-	--ACTTGACA	-AGCAGCAGC	TTGC--CCTC	AAGGT-GAC-	274
	C A G AT	A TG CA	CAG	C T C T	GGT GAC	
pGHV-gpB DNA.txt	AAACCAGTGT	CTCATTACAT	AAAAGTCTCA	GGCTTCTCAG	TGCATCGGAT	249
pGHV2 DNA.txt	-GTGCAATGC	GTT-TTAC--	---GGCTTCA	CGGGAGCC-G	TGCA-CGG-T	314
	CA TG T	TTAC	G TCA	G	C G TGCA	CGG T
pGHV-gpB DNA.txt	GAAAAGTGCT	TCTCTAGACC	TCCAGTGACA	TTTAAGTTTA	TGAATGACAG	299
pGHV2 DNA.txt	CTGCTGC-CG	TGTCT--CCC	TCTAGCGGCG	TCCA---TCA	CCAGC-ATAG	357
	G C T TCT	CC TC	AG G C	T A T A	A A AG	
pGHV-gpB DNA.txt	TACTATTTAC	AAAGGGCAAC	TAGGAGTCAA	TAATGAGATT	CTCTTAACCA	349
pGHV2 DNA.txt	GGC--GGGAC	A---TGC--T	TAGG---CA-	-GACGAG-TG	ACTTTATCAA	394
	C AC A	GC	TAGG CA	A GAG T	TTA C A	
pGHV-gpB DNA.txt	CAACATACCT	TGAAACATGT	CAGGAAAACA	CTGAGTATTA	CTTTCAGGCA	399
pGHV2 DNA.txt	CAATGT-CCT	T-----TCGT	CTAGAGAATA	CG-----	-----	420
	CAA T CCT T	GT C	GA AA A C			
pGHV-gpB DNA.txt	AAGACAGACA	TGTACATTTA	CAAAACTAT	GAGCATTTGA	AGACTGTGCC	449
pGHV2 DNA.txt	-----	-----	-----	-----	-----	420
pGHV-gpB DNA.txt	TTTATCTTCG	ATCACCACAC	TAGATACATT	TATAGCCCTT	AATTTTACAC	499
pGHV2 DNA.txt	-----	-----	-----	-----	-----	420
pGHV-gpB DNA.txt	TATTGGAGAA	TGTTGACTTT	AAAGTCATTG	AACTTTATAC	CAGGGACGAG	549
pGHV2 DNA.txt	-----	-----	-----	-----	-----	420
pGHV-gpB DNA.txt	AAGAGGCTTA	GTAATGTCTT	TGACATTGAA	ACAATG		585
pGHV2 DNA.txt	-----	-----	-----	-----		420



# Figure 7

pGHV-gpB prot	NLRIRINNIL EDLSKAWCRE QHRAALVWNE LSKINPTSVM SMIYNRPVSA	50
pGHV2 prot.txt	S--IMIANNL -----C-- --YSTLI--- LNDEDVTG-- -----IDE	25
	I I N L C L L T	
pGHV-gpB prot	KRIGDVISVS NCIVVDQTSV SLHKSILRLLS ASDEKCFSRP PVTFKFMNDS	100
pGHV2 prot.txt	K---DILTVH ---VNKNTV----- --YRFVRSS	45
	K D V V V F S	
pGHV-gpB prot	---TIYKQL GV-NNHILLT TTYLETQEN TEYFFQAKTD MYI---YKN-	142
pGHV2 prot.txt	VRESILGTLL SRWLRKRKEV KARMKRCEDP MLALILDKQQ LALKVTCNAF	95
	I L C K	
pGHV-gpB prot	YEHLKTVP-- LSSITTLDTF IALNFTLL-E NVDFKVIELY TRD---EK-R	185
pGHV2 prot.txt	YGFTGAVHGL LPCLPLAASI TSIGRDMRLQ TSDFINNVLS SREYVSEKFS	145
	Y V L L DF L R EK	
pGHV-gpB prot	LSNV-F--DI ETM-	195
pGHV2 prot.txt	LSDGDFQGDF SPEC	159
	LS F D	

Figure 8

pGHV-gpB DNA	AATCTTCGTA TCAGAATAAA TAACATTTTG GAAGATTTGT CAAAGGCATG	50
AF118399 DNA.txt	-----	
pGHV-gpB DNA	GTGTCGTGAG CAGCATAGAG CTGCTCTGGT GTGGAATGAG CTCAGCAAGA	100
AF118399 DNA.txt	-----	
pGHV-gpB DNA	TTAATCCAC AAGCGTCATG AGCATGATTT ACAATAGACC CGTATCAGCC	150
AF118399 DNA.txt	-----	
pGHV-gpB DNA	AAAAGAATAG GAGATGTCAT TTCAGTCTCT AACTGTATTG TGGTAGACCA	200
AF118399 DNA.txt	-----	
pGHV-gpB DNA	AACCAGTGTC TCATTACATA AAAGTCTCAG GCTTCTCAGT GCATCGGATG	250
AF118399 DNA.txt	-----	
pGHV-gpB DNA	AAAAGTGCTT CTCTAGACCT CCAGTGACAT TTAAGTTTAT GAATGACAGT	300
AF118399 DNA.txt	-----TAAT CTATGTCAC T AT ATG CA T	14
pGHV-gpB DNA	ACTATTTACA AAGGGCAACT AGGA-GTCAA TAATGAGATT CTCTTAACCA	349
AF118399 DNA.txt	-CTACCC-TA ATCCATCATG AAGACCTGCA TAAATATCCT CAATTAAAGG	62
	CTA A A A A GA T A TAA A T A TTAA	
pGHV-gpB DNA	CAACATACCT TGAAACATGT CAGGAAAACA CTGAGTATTA CTTTCAGGCA	399
AF118399 DNA.txt	AGGAGGATTA TGAAACAT-- -- -- --TTT--	83
	A TGAAACAT TTT	
pGHV-gpB DNA	AAGACAGACA TGTACATTTA CAAAACTAT GAGCATTGA AGACTGTGCC	449
AF118399 DNA.txt	-----TG---ATT-- -- -- --AG---TT-- --CTG---	95
	TG ATT AG TT CTG	
pGHV-gpB DNA	TTTATCTTCG ATCACCACAC TAGATACATT TATAGCCCTT AATTTTACAC	499
AF118399 DNA.txt	----- -- -- --GTCC-- -- -- --GTCC	99
pGHV-gpB DNA	TATTGGAGAA TGTTGACTTT -----AAAG TCAT-T--GA A---CTT---	534
AF118399 DNA.txt	-----TGTTCACTTT GTAAAAAAC ACATATCAGA ATCTCTTCTG	139
	TGTT ACTTT AAA CAT T GA A CTT	
pGHV-gpB DNA	--TA----- -TAC--CA-- G--GG--ACG AGA----- --AG--AGG-	555
AF118399 DNA.txt	TCTAACCTGC TTACAACATG GCTGGCTAAG AGAAAAATGA TCAGAAAGGA	189
	TA TAC CA G GG A G AGA AG AGG	
pGHV-gpB DNA	CTTAGTA--A TGT-CT--TT GACA-TTGA- AACATG--- -- -- --	585
AF118399 DNA.txt	ATTAGCAGCA TGTGCTGACC CAAAGCTCAG GACAAT-TTT AGATAAACAG	238
	TTAG A A TGT CT A A T A ACAAT	
pGHV-gpB DNA	-----	585
AF118399 DNA.txt	CAGCTTGCAA TTAAGGTGAC ATGCAATGCT GTGTATGGGT TCACTGGTGT	288
pGHV-gpB DNA	-----	585
AF118399 DNA.txt	TGCATCTGGT ATGCTGCCCT GTCTCAAGAT TGCAGAGACC ATAACATATGC	338
pGHV-gpB DNA	-----	585
AF118399 DNA.txt	AAGGAAGGGC CATGTTGGAA AAGACAAAAG TATTTGTAGA GAATTTAAGT	388
pGHV-gpB DNA	-----	585
AF118399 DNA.txt	CATGAGGATC TCCATTCCAT CTGTAAGGTT GGCTTTATGC CTCAGTCACC	438
pGHV-gpB DNA	-----	585
AF118399 DNA.txt	AAACAGCATT GATAAACCT TCAAGGTG	466

Figure 9

pGHV-gpB DNA	-----	-----	-----	-----	-----	
AF118401 DNA.txt	GAGGACCTGC	ATAAGTATCC	TCAATTAAAG	GAGGATGATT	ATGAAACATT	50
pGHV-gpB DNA	-----	-----	-----	---AATCTTC	GTATCAGAAT	17
AF118401 DNA.txt	TTTGATTAGT	TCTGGCCCTG	TTCACTTTGT	AAAAAAACAC	ATATCAGAAT	100
				AA C	TATCAGAAT	
pGHV-gpB DNA	AAATAACATT	TTGGAAGATT	TGTCAAAGGC	ATGGTGTCTG	GAGCAGCATA	67
AF118401 DNA.txt	-----C-TC	TT-----	-----	-----	-----	105
	C T	TT				
pGHV-gpB DNA	GAGCTGCTCT	GGTGTGGAAT	GAGCTCAGCA	AGATTAATCC	CACAAGCGTC	117
AF118401 DNA.txt	---CTG-TC-	-----GAA-	---CTT----	-G-----CT	CACAA-----C	125
	CTG TC	GAA	CT	G	C CACAA C	
pGHV-gpB DNA	ATGAGCATGA	TTTACAATAG	ACCCGTATCA	GCCAAAAGAA	-----T---	158
AF118401 DNA.txt	ATG-GC-TG-	-----	-----	GCCAAGAGAA	AAATGATCAG	152
	ATG GC TG				T	
pGHV-gpB DNA	--AGG-----	--AG-ATGT-	-----	-----CA	--TTT-----	172
AF118401 DNA.txt	AAAGGAATTG	ACAGCATGTG	CTGATCCAAA	GCTCAGGACA	ATTTTAGATA	202
	AGG	AG ATGT		CA	TTT	
pGHV-gpB DNA	-----CAGTC	T---CTA--	---AC-TGTA	TTG-TG-GTA	--GA-CCA--	200
AF118401 DNA.txt	AACAGCAGCT	TGCAATTAAAG	GTGACATGCA	ATGCTGTGTA	TGGATTCAC	252
	CAG T	TA	AC TG A	TG TG GTA	GA CA	
pGHV-gpB DNA	-----A-	-----AC-CA	G---TGCTC	A-----	-----TTAC	217
AF118401 DNA.txt	GGTGTTCAT	CTGGTATGCT	GCCATGTCTC	AAGATTGCAG	AGACCATCAC	302
	A	A C G	TGCTC A		TCAC	
pGHV-gpB DNA	-----	-----	-----AT	AAAAGT--CT	-CAG-GCTTC	235
AF118401 DNA.txt	TATGCAAGGA	AGGGCCATGT	TGGAAAAGAC	AAAAGTATTT	GTAGAGAATC	352
			A	AAAAGT T	AG G TC	
pGHV-gpB DNA	TCAG---TGC	A---TCGGA	T-GAAAAGT-	-GCTT--CTC	TAGACCTCCA	273
AF118401 DNA.txt	TGAGTCATGA	AGATCTCCGT	TCCATATGTA	AGGTGGCTC	TATACCTC-A	401
	T AG TG A	TC G	T A A GT	G TT CTC	TA ACCTC A	
pGHV-gpB DNA	GTGACATTTA	AGTTTATGAA	TGACAGTACT	ATTTACAAAG	GGCAACTAGG	323
AF118401 DNA.txt	GT--CA-TCA	A---ACG--	TG-----	-TTT-----	-----	417
	GT CA T A A	A G	TG	TTT		
pGHV-gpB DNA	AGTCAATAAT	GAGATTCTCT	TAACCACAAC	ATACCTTGAA	ACATGTCAGG	373
AF118401 DNA.txt	-G---ATAAA	-----	-----	-----	-----	423
	G ATAA					
pGHV-gpB DNA	AAAACACTGA	GTATTACTTT	CAGGCAAAGA	CAGACATGTA	CATTTACAAA	423
AF118401 DNA.txt	-----	-----	-----	-----	-----	423
pGHV-gpB DNA	AACTATGAGC	ATTTGAAGAC	TGTGCCTTTA	TCTTCGATCA	CCACACTAGA	473
AF118401 DNA.txt	-----	-----	-----	-----	-----	423
pGHV-gpB DNA	TACATTTATA	GCCCTTAATT	TTACACTATT	GGAGAATGTT	GACTTTAAAG	523
AF118401 DNA.txt	-----	-----	-----	-----	-----	423
pGHV-gpB DNA	TCATTGAACT	TTATACCAGG	GACGAGAAGA	GGCTTAGTAA	TGCTTTTGAC	573
AF118401 DNA.txt	-----	-----	-----	-----	-----	423
pGHV-gpB DNA	ATTGAAACAA	TG	585			
AF118401 DNA.txt	-----	--	423			

[illegible]

Score = 91.1 bits (47), Expect = 7e-16  
Identities = 117/152 (76%), Positives = 117/152 (76%)

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Figure 11(a)

gi|2337975 (AF005370) glycoprotein B [Alcelaphine herpesvirus 1]  
Length = 854

Score = 953 bits (2437), Expect = 0.0

Identities = 463/804 (57%), Positives = 589/804 (72%), Gaps = 26/804 (3%)

Query: 74 KNIYGSPSTFPYRVCSASGVGDVFRFQTDHVCPCDASDMVHSEGILLIYKQNIIPFMFRVR 133  
K I+ PS FP+RVCSAS +GD+FRFQT H CP+ D H+EGILLI+K+NI+P++F+VR  
Sbjct: 55 KGIHSDPSAFPFRVCSASNIGDIFRFQTSHPNTKDKHEGILLIFKENIVPYVFKVR 114

Query: 134 KYRKVVTSTTVYNGIYSDSITNQHTFYKSIPEWETEKMDTIYQCNSLRLNTGGNLLTYV 193  
KYRK+VTTST+YNGIY+D++TNQH F KS+ +ET +MDTIYQC+NSL + GGNLL Y  
Sbjct: 115 KYRKIVTSTTIYNGIYADAVTNQHVFSKSVPIYETRRMDTIYQCYNSLDVTVGGNLLVYT 174

Query: 194 DRDDINMTVFLQPVDGVTDPVKRYGSQPELYLEPGWFGSYRRRTTVNCELMDMFARSNP 253  
D D NMTV LQPVDG++ V+RY SQPE++ EPGW G YRRRTTVNCE+ + AR+ P  
Sbjct: 175 DNDGSNMTVDLQPDGLSNSVRRYHSQPEIHAEPGWLLGGYRRRTTVNCEVTETDARAVP 234

Query: 254 PFDFFVTATGDTVEMSPFWSGEDDHENKMHEKPWFVSVINNYKVVDYQNRGTVPLGKTRI 313  
PF +F+T GDT+EMSPFWS + E ++V +Y+VVDY+ RGT P G TRI  
Sbjct: 235 PFRYFITNIGDTIEMSPFWSKAWNETEFSGEPDRTLTVAKDYRVVDYKFRGTQPGHTRI 294

Query: 314 FLDREEYTLSEKHLKNMSYCPLTLWKAFYNGIQTEHSGSYHFVANDITASFTTSKEDMK 373  
F+D+EEYTLSEW + +N+SYC WK+F N I+TEH S HFVANDITASF T +  
Sbjct: 295 FVDKEEYTLSEWQQFRNISYCRWAHWKSFDAIKTEHGKSLHFVANDITASFYTPNTQTR 354

Query: 374 EFNTTYHCLNXXXXXXXXXXXXXXXXVNSTHSGYKDLKYFKTDGGLYLVWQPLIQNRLLDAKN 433  
E + CLN VN THS G +Y+ T+GGL LVWQPL+Q +LLDAK  
Sbjct: 355 EVLGKHVCLNNTIESELKSRLAKVNDTHSPNGTAQYYLTNGGLLLVWQPLVQKLLDAKG 414

Query: 434 KLN-----NETYSRRSRRQAESTTDPMMEMTGNGAGGEYSSENSITVAQVQYAYDN 484  
L+ T + RSRRQ S + +G Y++E++I + Q+Q+AYD  
Sbjct: 415 LLDVAVKKQNTTTTTTTTTTSRRRQRRSVS-----SGIDDVYTAESTILLTQIQFAYDT 466

Query: 485 LRIRINNILEDLKAWCREQHRAALVWNELSKINPTSVMSMIYNRPVSAKRIGDVISVSN 544  
LR +INN+LE+LS+AWCREQHRA+L+WNELSKINPTSVMS IY RPSAKRIGDVISVS+  
Sbjct: 467 LRAQINNVLLELSRAWCREQHRAALVWNELSKINPTSVMSIYGRPSAKRIGDVISVSH 526

Query: 545 CIVVDQTSVSLHKSRLLSA-SDEKCFSRPPVTFKFMNDSTIYKGQLGVNNEILLTTTYL 603  
C+VVDQ SVSLH+S+R+ +C+SRPPVTFKF+NDS +YKGQLGVNNEILLTTT +  
Sbjct: 527 CVVVDQDSVSLHRSRMRVPGRDKTHECYSRPPVTFKFINDSHLYKGQLGVNNEILLTTTAV 586

Query: 604 ETCQENTTEYFFQAKTDMYIYKNEYHLKTVPLSSITTLDTFIALNFTLLENVDFKVIELYT 663  
E C ENTE+YFQ +MY YKNY H+KT+P+ + TLDTF+ LN TL+EN+DF+VIELY+  
Sbjct: 587 EICHENTEYFQGGNNMYFYKNYRHVKTMPVGDVATLDTFMVLNLTLENIDFQVIELYS 646

Query: 664 RDEKRLSNVFDIETMFREYNYYAQRVSGLRKDLLDLSTNRNQFVDAFGSLMDDLGAVGQT 723  
R+EKR+S FDIETMFREYNYY QRV+GLR+DL DL+TNRNQFVDAFGSLMDDLGA VG+T  
Sbjct: 647 REEKRMSAFDIETMFREYNYYTQRTVGLRRDLTDLATNRNQFVDAFGSLMDDLGVVGKT 706

Figure 11(b)

Query: 724 VVNAVSGVATLFSSIVTGFINFIKNPFGGMLMIIVVIGVLF AIYFLT KKT KIYETAPIKM 783  
V+NAVS VATLFSSIV+G INFIKNPFGGML+ ++ V+ + L +K K + P++M  
Sbjct: 707 VLNAVSSVATLFSSIVSGIINFIKNPFGGMLLFGLIAAVVITVILLNRKAKRFAQNPVQM 766

Query: 784 IYPEIDKLKEREKSEIAPISEEEELERIVLAMHIHQONSHMETK-----TRKDPKDSI 836  
IYP+I + + + ++ PIS+ EL+RI+LAMH + + E+K T P D  
Sbjct: 767 IYPDIKTITSQREELQVDPISKHELDRIMLAMHDYHASKQPESKQDEEQGSTTSGPAD-W 825

Query: 837 LTRAQNMLRKRSYGYSNLKNAESVE 860  
L +A+N+LR+R+GY LK +S E  
Sbjct: 826 LNKAKNVLRRRAGYKPLKRTDSFE 849

Query: 837 LTRAQNMLRKRSYGYSNLKNAESVE 860  
L +A+N+LR+R+GY LK +S E  
Sbjct: 826 LNKAKNVLRRRAGYKPLKRTDSFE 849